

doest.co.caes



Figure 1 Nucleotide Sequence and predicted protein for HLTDG74

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-88	GTTGC	TCTG	GC/	AGC(CAA	GTT(GGC/	ATA	TTG	GAA	GCT	Ш	TCC	GGG	ת	rgg/	AGG/	AGG (3T-2	9
	CCCTGC	70							90 CAT	ccc	~~~	-	ccci		110			-67	-т	31
-28	CCCTGC	псп	ICC	IAC	AGC	LGI	ונני	יטטט	M	A	L I G	3C 11	יטטטי	30CI	316	1	H	. v	W	11
-8									ίΨΙ	~	"	_	u	^	,	_		•	••	
		130						1	50						170	9				
32	GGGGTT	CCT/	ΔΔΤ	CT	רהה	CAG	CTG			GGC	CAG	AGC	CCA	GCT	GGA	ΠC	TGA	TGG	CA	91
12	G W	L	M	L	G	S	c	L	L	A	R	A	Q	L	D	S	D	G	T	31
	•	_		_									_							
		190						2	10						230					454
92	CCATCA	CTATA	AGA(GGA	GCA	GAT	TGT	CCT	TGT	GCT	GAA	AGC	GAA	AGT/	ACA/	ATG	TGA	ACT	CA	151
32	IT	I	Ε	Ε	Q	Ι	٧	L	٧	L	K	A	K	٧	Q	C	E	L	N	51
		250						7	70						29	a				
. .	ACATCA	250	TCA	A C T	CCA	CGA	ccc	4 AGA	V.C.C	TAA	TTG	ш	רכר	TGA.			TGG	ΔCΤ	CA	211
152	I T	LAGC	100	AC II	~	F	GGG	F	ัด	N.	٠,٠	F	P	E	W	D	G	L	Ī	71
52	Τ.	-	Ų	_	Y	-	·	•	•	••		•	•	_						
		310						3	30						35					
212	TITGIT	GGCC	CAG	AGG	AAC	AGT	GGG	GAA	AAT	ATC	GGC	TGT	TCC	ATG	CCC	TCC	TTA	TAT	π	271
72	C W	P	R	G	T	٧	G	Κ	I.	S	A	٧	Ρ	C	Ρ	Ρ	Y	Ι	Υ	91
. –																_				
		370						3	90						41			cci		221
272				TAA	AGG	AGT	T.GC A	Щ	CCG	ACA	CTG	IAA	ונכנ	CAA	166	AAL	AIU	GGA	F	331 111
92	D F	N	Н	K	G	٧	A	۲	к	н	Ľ	N	۲	N	u	•	77	U	F	111
		430						A	50						47	a				
227	TTATGC	430 434	т	A A A	TAA	۸۸۵	ATG			TTA	TTC	AGA	ста	CCT			тст	GCA	.GC	391
332 112	M H	ACAG	1	~~~ N	K	T	w	Δ	N	Ϋ́	S	D	Ċ	L	R	F	Ĺ	Q	P	131
TTZ	(4) 11		-	•••		•	••	•			-							•		
		490						5	10						53					
392	CAGATA	TCAG	CAT	AGG	AAA	GCA	AGA	AΠ	CTO	TGA	ACG	icci	CTA	TGT	TAA	GT/	VTAC	์เต	ΤG	451
132	DI	-5	I	G	K	Q	Ε	F	C	Ε	R	L	Y	٧	M·	Y	T	٧	G	151
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452	GCTACT	CCAT	כזכ	$\overline{\Pi}$ 1	TGG	ıπα	.CH	660	- 161	660	.IĄI	110	ILAI	LAI	100	31 17	4C	D	R	171
152	Y S	Ι	2	F	G	5	L	A	٧	A	1	L	1	1	u	•	F	n	ĸ	71.7
		610							530						65	50				
512	GATTGC	ATTC OTO	י ראר	TAG	:GAA	(T	TAT	rcci	150 160	rgc I	ιсπ	AT	ПG	GTO			rgc	TGA (GAG	571
172	LH	A 1 1 0	T	R	N	Y	Ť	Н	M	Н	L	F	v	S	F	M	L	R	A	191
717	L II		•	-11	.,	•	-	••	• •	••	_	•	•	_						
		670)					(590							LØ				
572	CTACAA	GCAT	СП	TGI	CAA	VAG/	\CA(SAG	TAG	rcc	ATG(TC	ACAT	rag(AG	ΓΑΑ	AGG	AGC	TGG	631
192	T S		F	٧	K	D	R	٧	٧	H	A	Н	I	G	٧	K	Ε	L	Ε	211

325800-458

FIGURE 1 1/3

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COMPAND CAMEGO

632 212	AGTC	CT	730 AAT/ I	AAT(GCA(GA7	rga(CCC#	75 \CAA 0	ĀĀT	ПС(S	CAT	ΓGA(E	GGCA A	IACT	776 ГТСТ 5	GT	GAC D	AAA K	T S	691 231
692 232	CACA	ΔΤΔ'	790 TAT	GGG	πG	- AA(AT	rgcT	81 GTT	.0 GT(GAT	ST I	ΓΑΤ		770	830 CCTC) GCT	rac/	LAAT	Τ.	751 251
752 252	ΔΤΤΔ	TTG:	850 GAT(сто	எர	GGA/	\GG	TCTO	87 TAC	'0 :CT(GCA ⁻	TAA ⁻	rct(.11	898 TGT() GCT	rtt(П	811 271
812 272	CGGA	CAC	910	ΔΤΔ	· (T(TGC	igg	CTT	93 ATC	30	GAT	AGG	CTG		111	956 TCC/	3 AGC/	AGC/	ATT T	rg	871 291
872 292	TTGC	۸۵۲	970 ATG	sect	កោ	sec.	ACG/	AGC/	99 VACT	90 rct(GGC	TGA'	TGC		STG	1016 CTG	a GGA	ACT	TAG	rg.	931 311
932 312	CTGG/	۸GA	030 CAT	ΓΔΔΟ	STG(GAT	ГТА [*] Ү	TCA/ Q	105 AGC/ A	ACC	GAT I	cTI.	AGC A	AGC A	TAT	107(TGG(GCT	GAA' N	TTT F	TA I	991 331
992 332	ПСТ: L	σī	090 TCT: L	GAAT N	TAC	GGT V	TAG. R	AGT	111 TCT/ L	AGC	TAC T	CAA K	AAT I	CTG	GGA	1130 GAC	CAA'	TGC.	AGT . V	TG G	1051 351
1052 352	GGCA	TGA	150 CAC. T	AAG(GAA:	GCA. Q	ATA Y	CAG(R	117 GAA K	ACT	GGC A	CAA K	ATC S	GAC T	ACT	119 GGT V	сст	GGT V	сст L	AG V	1111 371
1112 372	TCTT F	TGG	210 AGT V	CC V.	TTA Y	CAT	CGT V	GTT(12: CGT(V	GTG	ככד נ	GCC P	TCA H	וכדכ S	сп F	125 CAC T	TGG	GCT L	cee	GT W	1171 391
1172 392	GGGA E	GAT	270 CCG R	CAT	GCA H	ста С	TGA E	GCT	12: CTT: F	ĊП	CAA	CTC S	:CT1	TCA Q	.GGC	131 111 F	m	TGT V	ज ऽ	TA I	1231 411
1222	TCAT	1	330 CTG	CTA	CTG	CAA	TGG	AGA	13 ബേ	50 TCA	ເດດເ	'AGA	เดตา	rgaa	GA/	137 AGAT	'0 'दा	GAG	at Co	igt	1291 431
1797	GGAA N	1 TC	.390 .CTC	์เส	GGA	ста	GAA	AAĠ	14 GAC	10 ACC	:GC(ATO	τGC	CAG	icco	143 GCAC	Ø ATC	CGC	CTC	AG	
	TGCT	CAC	.450 CAC	сст	GAC	GCA	CAG	icac	14 CAG	70 CAC	scc/	AGTO	CAC		rggi	149 CGG(90 CAG(CAC	ACGO		1411 471
732	-		.510					80	15	30			`		4	15					
				<u></u>					F	4		0	' ₇					9	9 }	9	

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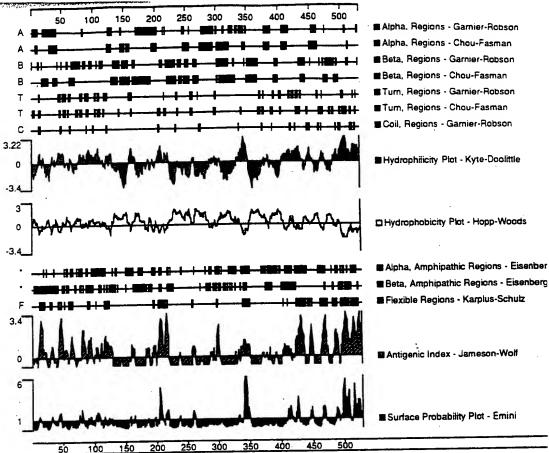
1412 GGTGCTTATCTCTGGCAAAGCTGCCAAGATCGCCAGCAGACAGCCTGACAGCCACATCAC 472 C L S L A K L P R S P A D S L T A T S L	491
1570 1590 1610 1472 TTTACCTGGCTATGTCTGGAGTAACTCAGAGCAGGACTGCCTCACACACTCTCTCCACGA 492 Y L A M S G V T Q S R T A S H T L S T R	1531 511
1630 1650 1670 1532 GGAGCAACAAGGAAGATAGTGGGAGGCAGAGAGATATTCTAATGGAGAAGCCTTCCA 512 S N K E D S G R Q R D D I L M E K P S R	1591 531
1690 1710 1730 1592 GGCCTATGGAATCTAACCCAGACACTGAAGGATGACAAGGAGAAACTGAGGATGTTCTCT 532 P M E S N P D T E G	1651 541
1750 1770 1790 1652 GAATGGACATGTGTGGCTGACTTTCATGGGCTGGTCCAATGGCTGGTTGTGAGAGAGGGC	1711
1810 1830 1850 1712 TTGGCTGATACTCCTATGCTTGAGCACAAAGGCTGAAAATTCAGTTAAGGTGTTACTTAA	1771
1870 1890 1910 1772 TAATAGTTTTTAGGCTCCATGAATTGGCTCCTGTAAATACTAACGACATGAAAATGCAAG	1831
1930 1950 1970 1832 TGTCAATGGAGTAGTTTATTACCTTCTATTGGCATCAAGTTTTCCTCTAAATTAATGTAT	1891
1990 1892 GGTATTTGCTCTGTGATTGTTCA	1914

325800-458 FIGURE 1 3/3



3010





325800-458 FIGURE 2 1/1

4016



High Probability .. Score P(N. S.2e-20∔ 597 2.9e-203 580 6.7e-190 580 6.le-189 .7e-188 576 576 7.7e-188

Readi

parathyroid hormone receptor [Di... +3 gp M74445 IOPOPTHR_1 parathyroid hormone / parathyroi... +3 pirISIA39286 parathyroid hormone receptor [Ho... +3 gp|L04308|HUMPTHR_1 parathyroid hormone receptor - h... +3 pir|S|S29610 gp|M77184|RATPATHYR_1 parathyroid hormone receptor [Ra... +3 parathyroid hormone/parathyroid ... +3 gp | X78936 | MMPHRPP_1 576 parathyroid hormone and parathyr... +3 7.7e-188 pir|5|A42698 gp|L34611|MUSPTHR06_1 parathyroid hormone/parathyroid ... +3 576 4.le-174 1.2e-98 gp!U11087|HSV1RG9_1 · vasoactive intestinal peptide 1 ... +3 gp|M86835|RATVASREC_1 vasoactive intestinal polypeptid... +3 254 3.1e-91

WARNING: Descriptions of 49 database sequences were not reported due to the limiting value of parameter V = 10.

>gp!M74445!OPOPTHR_1 parathyroid hormone receptor [Didelphis virginiana] Length = 585

Plus Strand HSPs:

Score = 597 (274.6 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204Identities = 108/172 (62%), Positives = 136/172 (79%), Frame = +3

729 IMQDDPQNSIEATSVDKSQYIGCKIAVVMFIYFLATNYYWILVEGLYLHNLIFVAFFSDT 908 Ü Ouerv: DK+ ++GC++AV +F+YFL TNYYWILVEGLYLH+LIF+AFFS+ I +++ + E 253 ITEEFLRAFTEPPPADKAGFVGCRVAVTVFLYFLTTNYYWILVEGLYLHSLIFMAFFSEK 312 ĩΨ Sbjct:

909 KYLWGFILIGWGFPAAFVAAWAVARATLADARCWELSAGDIKWIYQAPILAAIGLNFILF 1088 Ouery: KYLWGF L GWG PA FVA W RATLA+ CW+LS+G+ KWI Q PILAAI +NFILF 313 KYLWGFTLFGWGLPAVFVAVWVTVRATLANTECWDLSSGNKKWIIQVPILAAIVVNFILF 372 Sbict:

1089 LNTVRVLATKIWETNAVGHDTRKQYRKLAKSTLVLVLVFGVHYIVFVCLPHS 1244 Query: +N +RVLATK+ ETNA DTR+QYRKL KSTLVL+ +FGVHYIVF+ P++ 373 INIIRVLATKLRETNAGRCDTRQQYRKLLKSTLVLMPLFGVHYIVFMATPYT 424 Sbict:

Score = 284 (130.6 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204Identities = 42/70 (60%), Positives = 55/70 (78%), Frame = +3

267 EGNCFPEWDGLICWPRGTVGKISAVPCPPYIYDFNHKGVAFRHCNPNGTWDFMHSLNKTW 446 +G C PEWD ++CWP G GK+ AVPCP YIYDFNHKG A+R C+ NG+W+ + N+TW Ouerv: 102 DGFCLPEWDNIVCWPAGVPGKVVAVPCPDYIYDFNHKGRAYRRCDSNGSWELVPGNNRTW 161 Sbjct:

447 ANYSDCLRFL 476 Ouery: ANYS+C++FL 162 ANYSECVKFL 171 Sbict:

Score = 279 (128.3 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204 Identities = 51/81 (62%), Positives = 67/81 (82%), Frame = +3

498 KQEFCERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNYIHMHLFVSFMLRATSIFV 677 ++E +RL ++YTVGYSIS GSL VA+LI+GYFRRLHCTRNYIHMHLFVSFMLRA SIF+ 177 EREVFDRLGMIYTVGYSISLGSLTVAVLILGYFRRLHCTRNYIHMHLFVSFMLRAVSIFI 236 Sbict:

678 KDRVVHAHIGVKELESLIMOD 740 Ouery: KD V+++ + E+E + ++ 237 KDAVLYSGVSTDEIERITEEE 257 Sbict:

Score = 232 (106.7 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204Identities = 38/59 (64%), Positives = 50/59 (84%), Frame = +3

1248 TGLGWEIRMHCELFFNSFQGFFVSIIYCYCNGEVQAEVKRMWSRWNLSVDWKRTPPCGS 1424

325860

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Sbjct:

Score = 72 (33.1 bits). Expect = 8.2e-204, Sum P(6) = 8.2e-204 Identities = 16/37 (43%), Positives = 23/37 (62%), Frame = +3

159 AQLDSDGTITIEEQIVLVLKAKVQCELNITAQLQEGE 269 A +D+D IT EEQI+L+ A+ QCE + L+ E 24 ALVDADDVITKEEQIILLRNAQAQCEQRLKEVLRVPE 60 Query:

Score = 39 (17.9 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204 Identities = 9/23 (39%), Positives = 12/23 (52%), Frame = +2

Query: 1508 ISGKAAKIASRQPDSHITLPGYV 1576 +S + A A + H LPGYV Sbjct: 512 LSPRLAPGAGASANGHHQLPGYV 534

> 2/2 325800-458 FIGURE